

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5       (i) APPLICANT: Godowski, Paul J.  
                                Mark, Melanie R.  
                                Scadden, David T.  
                                Baker; Kevin P.  
                                Baron, Will F.
- 10       (ii) TITLE OF INVENTION: Protein Tyrosine Kinases
- (iii) NUMBER OF SEQUENCES: 35
- 15       (iv) CORRESPONDENCE ADDRESS:  
              (A) ADDRESSEE: Genentech, Inc.  
              (B) STREET: 460 Point San Bruno Blvd  
              (C) CITY: South San Francisco  
              (D) STATE: California  
20       (E) COUNTRY: USA  
              (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:  
              (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
25       (B) COMPUTER: IBM PC compatible  
              (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
              (D) SOFTWARE: patin (Genentech)
- (vi) CURRENT APPLICATION DATA:  
30       (A) APPLICATION NUMBER:  
              (B) FILING DATE: 23-NOV-1993  
              (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
35       (A) APPLICATION NUMBER:  
              (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
40       (A) NAME: Hasak, Janet E.  
              (B) REGISTRATION NUMBER: 28,616  
              (C) REFERENCE/DOCKET NUMBER: 854
- (ix) TELECOMMUNICATION INFORMATION:  
45       (A) TELEPHONE: 415/225-1896  
              (B) TELEFAX: 415/952-9881  
              (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

- 50       (i) SEQUENCE CHARACTERISTICS:  
              (A) LENGTH: 3611 bases  
              (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5  
CCGCCGATGG CGCTGAGGCG GAGCATGGGG CGGCCGGGGC TCCCGCCGCT 50  
10  
GCCGCTGCCG CCGCCACCGC GGCTCGGGCT GCTGCTGGCG GCTCTGGCTT 100  
CTCTGCTGCT CCCGGAGTCC GCCGCCGCAG GTCTGAAGCT CATGGGAGCC 150  
15  
CCGGTGAAGC TGACAGTGTC TCAGGGGCAG CCGGTGAAGC TCAACTGCAG 200  
TGTGGAGGGG ATGGAGGAGC CTGACATCCA GTGGGTGAAG GATGGGGCTG 250  
20  
TGGTCCAGAA CTTGGACCAG TTGTACATCC CAGTCAGCGA GCAGCACTGG 300  
25  
ATCGGCTTCC TCAGCCTGAA GTCAGTGGAG CGCTCTGACG CCGGCCGGTA 350  
CTGGTGCCAG GTGGAGGATG GGGGTGAAAC CGAGATCTCC CAGCCAGTGT 400  
30  
GGCTCACGGT AGAAGGTGTG CCATTTTTC AAGTGGAGCC AAAAGATCTG 450  
GCAGTGCCAC CCAATGCCCC TTTCCTACTG TCTTGTGAGG CTGTGGGTCC 500  
35  
CCCTGAACCT GTTACCATTG TCTGGTGGAG AGGAACTACG AAGATCGGGG 550  
40  
GACCCGCTCC CTCTCCATCT GTTTTAAATG TAACAGGGGT GACCCAGAGC 600  
ACCATGTTTT CCTGTGAAGC TCACAACCTA AAAGGCCTGG CCTCTTCTCG 650  
45  
CACAGCCACT GTTCACCTTC AAGCACTGCC TGCAGCCCCC TTCAACATCA 700  
CCGTGACAAA GCTTTCCAGC AGCAACGCTA GTGTGGCCTG GATGCCAGGT 750  
50  
GCTGATGGCC GAGCTCTGCT ACAGTCCTGT ACAGTTCAGG TGACACAGGC 800

CCCAGGAGGC TGGGAAGTCC TGGCTGTTGT GGTCCCTGTG CCCCCCTTTA 850  
 5 CCTGCCTGCT CCGGGACCTG GTGCCTGCCA CCAACTACAG CCTCAGGGTG 900  
 CGCTGTGCCA ATGCCTTGGG GCCCTCTCCC TATGCTGACT GGGTGCCCTT 950  
 10 TCAGACCAAG GGTCTAGCCC CAGCCAGCGC TCCCCAAAAC CTCCATGCCA 1000  
 TCCGCACAGA TTCAGGCCTC ATCTTGGAGT GGAAGAAGT GATCCCCGAG 1050  
 15 GCCCCTTTGG AAGGCCCCCT GGGACCCTAC AACTGTCCT GGGTTCAAGA 1100  
 20 CAATGGAACC CAGGATGAGC TGACAGTGA GGGGACCAGG GCCAATTGA 1150  
 CAGGCTGGGA TCCCCAAAAG GACCTGATCG TACGTGTGTG CGTCTCCAAT 1200  
 25 GCAGTTGGCT GTGGACCCTG GAGTCAGCCA CTGGTGGTCT CTTCTCATGA 1250  
 CCGTGCAGGC CAGCAGGGCC CTCCTCACAG CCGCACATCC TGGGTACCTG 1300  
 30 TGGTCCTTGG TGTGCTAACG GCCCTGGTGA CGGCTGCTGC CCTGGCCCTC 1350  
 35 ATCCTGCTTC GAAAGAGACG GAAAGAGACG CGGTTTGGGC AAGCCTTTGA 1400  
 CAGTGTCATG GCCCGGGGAG AGCCAGCCGT TCACTTCCGG GCAGCCCGGT 1450  
 40 CCTTCAATCG AGAAAGGCCC GAGCGCATCG AGGCCACATT GGACAGCTTG 1500  
 GGCATCAGCG ATGAACTAAA GGAAAACTG GAGGATGTGC TCATCCCAGA 1550  
 45 GCAGCAGTTC ACCCTGGGCC GGATGTTGGG CAAAGGAGAG TTTGGTTCAG 1600  
 50 TGCGGGAGGC CCAGCTGAAG CAAGAGGATG GCTCCTTTGT GAAAGTGGCT 1650

GTGAAGATGC TGAAAGCTGA CATCATTGCC TCAAGCGACA TTGAAGAGTT 1700  
 5 CCTCAGGGAA GCAGCTTGCA TGAAGGAGTT TGACCATCCA CACGTGGCCA 1750  
 AACTTGTGG GGTAAGCCTC CGGAGCAGGG CTAAAGGCCG TCTCCCCATC 1800  
 10 CCCATGGTCA TCTTGCCCTT CATGAAGCAT GGGGACCTGC ATGCCTTCCT 1850  
 GCTCGCCTCC CGGATTGGGG AGAACCCTT TAACCTACCC CTCCAGACCC 1900  
 15 TGATCCGGTT CATGGTGGAC ATTGCCTGCG GCATGGAGTA CCTGAGCTCT 1950  
 CGGAACCTCA TCCACCGAGA CCTGGCTGCT CGGAATTGCA TGCTGGCAGA 2000  
 20 GGACATGACA GTGTGTGTGG CTGACTTCGG ACTCTCCCGG AAGATCTACA 2050  
 25 GTGGGGACTA CTATCGTCAA GGCTGTGCCT CCAAAGTCC TGTCAAGTGG 2100  
 CTGGCCCTGG AGAGCCTGGC CGACAACCTG TATACTGTGC AGAGTGACGT 2150  
 30 GTGGGCGTTC GGGGTGACCA TGTGGGAGAT CATGACACGT GGGCAGACGC 2200  
 CATATGCTGG CATCGAAAAC GCTGAGATTT ACAACTACCT CATTGGCGGG 2250  
 35 AACCGCCTGA AACAGCCTCC GGAGTGTATG GAGGACGTGT ATGATCTCAT 2300  
 40 GTACCAGTGC TGGAGTGCTG ACCCCAAGCA GCGCCCGAGC TTTACTTGTC 2350  
 TGCGAATGGA ACTGGAGAAC ATCTTGGGCC AGCTGTCTGT GCTATCTGCC 2400  
 45 AGCCAGGACC CCTTATACAT CAACATCGAG AGAGCTGAGG AGCCCACTGC 2450  
 GGGAGGCAGC CTGGAGCTAC CTGGCAGGGA TCAGCCCTAC AGTGGGGCTG 2500  
 50 GGGATGGCAG TGGCATGGGG GCAGTGGGTG GCACTCCCAG TGA CTGTCTGG 2550

TACATACTCA CCCCCGGAGG GCTGGCTGAG CAGCCAGGGC AGGCAGAGCA 2600  
 5 CCAGCCAGAG AGTCCCCTCA ATGAGACACA GAGGCTTTTG CTGCTGCAGC 2650  
 AAGGGCTACT GCCACACAGT AGCTGTTAGC CCACAGGCAG AGGGCATCGG 2700  
 10 GGCCATTTGG CCGGCTCTGG TGGCCACTGA GCTGGCTGAC TAAGCCCCGT 2750  
 CTGACCCCAG CCCAGACAGC AAGGTGTGGA GGCTCCTGTG GTAGTCCTCC 2800  
 15 CAAGCTGTGC TGGGAAGCCC GGA CTGACCA AATCACC CAA TCCAGTTCT 2850  
 20 TCCTGCAACC ACTCTGTGGC CAGCCTGGCA TCAGTTTAGG CCTTGGCTTG 2900  
 ATGGAAGTGG GCCAGTCCTG GTTGTCTGAA CCCAGGCAGC TGGCAGGAGT 2950  
 25 GGGGTGGTTA TGTTTCCATG GTTACCATGG GTGTGGATGG CAGTGTGGGG 3000  
 AGGGCAGGTC CAGCTCTGTG GGCCCTACCC TCCTGCTGAG CTGCCCCTGC 3050  
 30 TGCTTAAGTG CATGCATTGA GCTGCCTCCA GCCTGGTGGC CCAGCTATTA 3100  
 CCACACTTGG GGTTTAAATA TCCAGGTGTG CCCCTCCAAG TCACAAAGAG 3150  
 ATGTCCTTGT AATATTCCCT TTTAGGTGAG GGTGTAAG GGGTTGGTAT 3200  
 40 CTCAGGTCTG AATCTTCACC ATCTTTCTGA TTCCGCACCC TGCCTACGCC 3250  
 AGGAGAAGTT GAGGGGAGCA TGCTTCCTG CAGCTGACCG GGTCACACAA 3300  
 45 AGGCATGCTG GAGTACCCAG CCTATCAGGT GCCCTCTTC CAAAGGCAGC 3350  
 50 GTGCCGAGCC AGCAAGAGGA AGGGGTGCTG TGAGGCTTGC CCAGGAGCAA 3400

GTGAGGCCCGG AGAGGAGTTC AGGAACCCTT CTCCATACCC ACAATCTGAG 3450

CACGCTACCA AATCTCAAAA TATCCTAAGA CTAACAAAGG CAGCTGTGTC 3500

TGAGCCCAAC CCTTCTAAAC GGTGACCTTT AGTGCCAACT TCCCCTCTAA 3550

CTGGACAGCC TCTTCTGTCC CAAGTCTCCA GAGAGAAATC AGGCCTGATG 3600

AGGGGGAATT C 3611

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 890 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Arg Arg Ser Met Gly Arg Pro Gly Leu Pro Pro Leu  
1 5 10 15

Pro Leu Pro Pro Pro Pro Arg Leu Gly Leu Leu Leu Ala Ala Leu  
20 25 30

Ala Ser Leu Leu Leu Pro Glu Ser Ala Ala Ala Gly Leu Lys Leu  
35 40 45

Met Gly Ala Pro Val Lys Leu Thr Val Ser Gln Gly Gln Pro Val  
50 55 60

Lys Leu Asn Cys Ser Val Glu Gly Met Glu Glu Pro Asp Ile Gln  
65 70 75

Trp Val Lys Asp Gly Ala Val Val Gln Asn Leu Asp Gln Leu Tyr  
80 85 90

Ile Pro Val Ser Glu Gln His Trp Ile Gly Phe Leu Ser Leu Lys  
95 100 105

Ser Val Glu Arg Ser Asp Ala Gly Arg Tyr Trp Cys Gln Val Glu  
110 115 120

Asp Gly Gly Glu Thr Glu Ile Ser Gln Pro Val Trp Leu Thr Val  
125 130 135

	Glu Gly Val Pro Phe Phe Thr Val Glu Pro Lys Asp Leu Ala Val	140	145	150
5	Pro Pro Asn Ala Pro Phe Gln Leu Ser Cys Glu Ala Val Gly Pro	155	160	165
	Pro Glu Pro Val Thr Ile Val Trp Trp Arg Gly Thr Thr Lys Ile	170	175	180
10	Gly Gly Pro Ala Pro Ser Pro Ser Val Leu Asn Val Thr Gly Val	185	190	195
	Thr Gln Ser Thr Met Phe Ser Cys Glu Ala His Asn Leu Lys Gly	200	205	210
15	Leu Ala Ser Ser Arg Thr Ala Thr Val His Leu Gln Ala Leu Pro	215	220	225
	Ala Ala Pro Phe Asn Ile Thr Val Thr Lys Leu Ser Ser Ser Asn	230	235	240
20	Ala Ser Val Ala Trp Met Pro Gly Ala Asp Gly Arg Ala Leu Leu	245	250	255
	Gln Ser Cys Thr Val Gln Val Thr Gln Ala Pro Gly Gly Trp Glu	260	265	270
	Val Leu Ala Val Val Val Pro Val Pro Pro Phe Thr Cys Leu Leu	275	280	285
30	Arg Asp Leu Val Pro Ala Thr Asn Tyr Ser Leu Arg Val Arg Cys	290	295	300
	Ala Asn Ala Leu Gly Pro Ser Pro Tyr Ala Asp Trp Val Pro Phe	305	310	315
	Gln Thr Lys Gly Leu Ala Pro Ala Ser Ala Pro Gln Asn Leu His	320	325	330
40	Ala Ile Arg Thr Asp Ser Gly Leu Ile Leu Glu Trp Glu Glu Val	335	340	345
	Ile Pro Glu Ala Pro Leu Glu Gly Pro Leu Gly Pro Tyr Lys Leu	350	355	360
45	Ser Trp Val Gln Asp Asn Gly Thr Gln Asp Glu Leu Thr Val Glu	365	370	375
	Gly Thr Arg Ala Asn Leu Thr Gly Trp Asp Pro Gln Lys Asp Leu	380	385	390

	Ile Val Arg Val Cys Val Ser Asn Ala Val Gly Cys Gly Pro Trp	395	400	405
5	Ser Gln Pro Leu Val Val Ser Ser His Asp Arg Ala Gly Gln Gln	410	415	420
	Gly Pro Pro His Ser Arg Thr Ser Trp Val Pro Val Val Leu Gly	425	430	435
10	Val Leu Thr Ala Leu Val Thr Ala Ala Ala Leu Ala Leu Ile Leu	440	445	450
	Leu Arg Lys Arg Arg Lys Glu Thr Arg Phe Gly Gln Ala Phe Asp	455	460	465
15	Ser Val Met Ala Arg Gly Glu Pro Ala Val His Phe Arg Ala Ala	470	475	480
	Arg Ser Phe Asn Arg Glu Arg Pro Glu Arg Ile Glu Ala Thr Leu	485	490	495
20	Asp Ser Leu Gly Ile Ser Asp Glu Leu Lys Glu Lys Leu Glu Asp	500	505	510
	Val Leu Ile Pro Glu Gln Gln Phe Thr Leu Gly Arg Met Leu Gly	515	520	525
25	Lys Gly Glu Phe Gly Ser Val Arg Glu Ala Gln Leu Lys Gln Glu	530	535	540
30	Asp Gly Ser Phe Val Lys Val Ala Val Lys Met Leu Lys Ala Asp	545	550	555
	Ile Ile Ala Ser Ser Asp Ile Glu Glu Phe Leu Arg Glu Ala Ala	560	565	570
35	Cys Met Lys Glu Phe Asp His Pro His Val Ala Lys Leu Val Gly	575	580	585
	Val Ser Leu Arg Ser Arg Ala Lys Gly Arg Leu Pro Ile Pro Met	590	595	600
40	Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ala Phe Leu	605	610	615
45	Leu Ala Ser Arg Ile Gly Glu Asn Pro Phe Asn Leu Pro Leu Gln	620	625	630
	Thr Leu Ile Arg Phe Met Val Asp Ile Ala Cys Gly Met Glu Tyr	635	640	645
50				



	Leu Ser Ser Arg	Asn Phe Ile His Arg	Asp Leu Ala Ala Arg	Asn
		650	655	660
5	Cys Met Leu Ala	Glu Asp Met Thr Val	Cys Val Ala Asp Phe	Gly
		665	670	675
	Leu Ser Arg Lys	Ile Tyr Ser Gly Asp	Tyr Tyr Arg Gln Gly	Cys
		680	685	690
10	Ala Ser Lys Leu	Pro Val Lys Trp Leu	Ala Leu Glu Ser Leu	Ala
		695	700	705
	Asp Asn Leu Tyr	Thr Val Gln Ser Asp	Val Trp Ala Phe Gly	Val
		710	715	720
15	Thr Met Trp Glu	Ile Met Thr Arg Gly	Gln Thr Pro Tyr Ala	Gly
		725	730	735
	Ile Glu Asn Ala	Glu Ile Tyr Asn Tyr	Leu Ile Gly Gly Asn	Arg
20		740	745	750
	Leu Lys Gln Pro	Pro Glu Cys Met Glu	Asp Val Tyr Asp Leu	Met
		755	760	765
25	Tyr Gln Cys Trp	Ser Ala Asp Pro Lys	Gln Arg Pro Ser Phe	Thr
		770	775	780
	Cys Leu Arg Met	Glu Leu Glu Asn Ile	Leu Gly Gln Leu Ser	Val
		785	790	795
30	Leu Ser Ala Ser	Gln Asp Pro Leu Tyr	Ile Asn Ile Glu Arg	Ala
		800	805	810
	Glu Glu Pro Thr	Ala Gly Gly Ser Leu	Glu Leu Pro Gly Arg	Asp
35		815	820	825
	Gln Pro Tyr Ser	Gly Ala Gly Asp Gly	Ser Gly Met Gly Ala	Val
		830	835	840
40	Gly Gly Thr Pro	Ser Asp Cys Arg Tyr	Ile Leu Thr Pro Gly	Gly
		845	850	855
	Leu Ala Glu Gln	Pro Gly Gln Ala Glu	His Gln Pro Glu Ser	Pro
		860	865	870
45	Leu Asn Glu Thr	Gln Arg Leu Leu Leu	Leu Gln Gln Gly Leu	Leu
		875	880	885
50	Pro His Ser Ser	Cys		
		890		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3637 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCTCGA GTCGACGTTG GACTTGAAGG AATGCCAAGA GATGCTGCCC 50  
CCACCCCCTT AGGCCCCGAGG GATCAGGAGC TATGGGACCA GAGGCCCTGT 100  
CATCTTTACT GCTGCTGCTC TTGGTGGCAA GTGGAGATGC TGACATGAAG 150  
GGACATTTTG ATCCTGCCAA GTGCCGCTAT GCCCTGGGCA TGCAGGACCG 200  
GACCATCCCA GACAGTGACA TCTCTGCTTC CAGCTCCTGG TCAGATTCCA 250  
CTGCCGCCCG CCACAGCAGG TTGGAGAGCA GTGACGGGGA TGGGGCCTGG 300  
TGCCCCGCAG GGTCGGTGTT TCCAAGGAG GAGGAGTACT TGCAGGTGGA 350  
TCTACAACGA CTGCACCTGG TGGCTCTGGT GGGCACCCAG GGACGGCATG 400  
CCGGGGGCCT GGGCAAGGAG TTCTCCCGGA GCTACCGGCT GCGTTACTCC 450  
CGGGATGGTC GCCGCTGGAT GGGCTGGAAG GACCGCTGGG GTCAGGAGGT 500  
GATCTCAGGC AATGAGGACC CTGAGGGAGT GGTGCTGAAG GACCTTGGGC 550  
CCCCCATGGT TGCCCGACTG GTTCGCTTCT ACCCCCGGGC TGACCGGGTC 600  
ATGAGCGTCT GTCTGCGGGT AGAGCTCTAT GGCTGCCTCT GGAGGGATGG 650  
ACTCCTGTCT TACACCGCCC CTGTGGGGCA GACAATGTAT TTATCTGAGG 700

CCGTGTACCT CAACGACTCC ACCTATGACG GACATACCGT GGGCGGACTG 750  
 CAGTATGGGG GTCTGGGCCA GCTGGCAGAT GGTGTGGTGG GGCTGGATGA 800  
 5 CTTTAGGAAG AGTCAGGAGC TGCGGGTCTG GCCAGGCTAT GACTATGTGG 850  
 GATGGAGCAA CCACAGCTTC TCCAGTGGCT ATGTGGAGAT GGAGTTTGAG 900  
 TTTGACCGGC TGAGGGCCTT CCAGGCTATG CAGGTCCACT GTAACAACAT 950  
 15 GCACACGCTG GGAGCCCGTC TGCCTGGCGG GGTGGAATGT CGCTTCCGGC 1000  
 GTGGCCCTGC CATGGCCTGG GAGGGGGAGC CCATGCGCCA CAACCTAGGG 1050  
 20 GGCAACCTGG GGGACCCAG AGCCCGGGCT GTCTCAGTGC CCCTTGGCGG 1100  
 CCGTGTGGCT CGCTTTCTGC AGTGCCGCTT CCTCTTTGCG GGGCCCTGGT 1150  
 TACTCTTCAG CGAAATCTCC TTCATCTCTG ATGTGGTGAA CAATTCCTCT 1200  
 30 CCGGCACTGG GAGGCACCTT CCCGCCAGCC CCCTGGTGGC CGCCTGGCCC 1250  
 ACCTCCCACC AACTTCAGCA GCTTGGAGCT GGAGCCCAGA GGCCAGCAGC 1300  
 35 CCGTGGCCAA GCCCGAGGGG AGCCCGACCG CCATCCTCAT CGGCTGCCTG 1350  
 GTGGCCATCA TCCTGCTCCT GCTGCTCATC ATTGCCCTCA TGCTCTGGCG 1400  
 GCTGCACTGG CGCAGGCTCC TCAGCAAGGC TGAACGGAGG GTGTTGGAAG 1450  
 45 AGGAGCTGAC GGTTCACCTC TCTGTCCCTG GGGACACTAT CCTCATCAAC 1500  
 AACCGCCCAG GTCCTAGAGA GCCACCCCG TACCAGGAGC CCCGGCCTCG 1550  
 50 TGGGAATCCG CCCCACTCCG CTCCTGTGT CCCCAATGGC TCTGCGTTGC 1600

TGCTCTCCAA TCCAGCCTAC CGCCTCCTTC TGGCCACTTA CGCCCGTCCC 1650  
 5 CCTCGAGGCC CGGGCCCCCC CACACCCGCC TGGGCCAAAC CCACCAACAC 1700  
 CCAGGCCTAC AGTGGGGACT ATATGGAGCC TGAGAAGCCA GGCGCCCCGC 1750  
 10 TTCTGCCCCC ACCTCCCCAG AACAGCGTCC CCCATTATGC CGAGGCTGAC 1800  
 ATTGTTACCC TGCAGGGCGT CACCGGGGGC AACACCTATG CTGTGCCTGC 1850  
 15 ACTGCCCCCA GGGGCAGTCG GGGATGGGCC CCCCAGAGTG GATTTCCTC 1900  
 20 GATCTCGACT CCGCTTCAAG GAGAAGCTTG GCGAGGGCCA GTTTGGGGAG 1950  
 GTGCACCTGT GTGAGGTCGA CAGCCCTCAA GATCTGGTCA GTCTTGATTT 2000  
 25 CCCCETTAAT GTGCGTAAGG GACACCCTTT GCTGGTAGCT GTCAAGATCT 2050  
 TACGGCCAGA TGCCACCAAG AATGCCAGGA ATGATTTCTT GAAAGAGGTG 2100  
 30 AAGATCATGT CGAGGCTCAA GGACCCAAAC ATCATTCGGC TGCTGGGCGT 2150  
 35 GTGTGTGCAG GACGACCCCC TCTGCATGAT TACTGACTAC ATGGAGAACG 2200  
 GCGACCTCAA CCAGTTCCTC AGTGCCCACC AGCTGGAGGA CAAGGCAGCC 2250  
 40 GAGGGGGCCC CTGGGGACGG GCAGGCTGCG CAGGGGCCCA CCATCAGCTA 2300  
 CCCAATGCTG CTGCATGTGG CAGCCCAGAT CGCCTCCGGC ATGCGCTATC 2350  
 45 TGGCCACACT CAACTTTGTA CATCGGGACC TGGCCACGCG GAACTGCCTA 2400  
 50 GTTGGGGAAA ATTCACCAT CAAAATCGCA GACTTTGGCA TGAGCCGGAA 2450

CCTCTATGCT GGGGACTATT ACCGTGTGCA GGGCCGGGCA GTGCTGCCCCA 2500  
 5 TCCGCTGGAT GGCCTGGGAG TGCATCCTCA TGGGGAAGTT CACGACTGCG 2550  
 AGTGACGTGT GGGCCTTTGG TGTGACCCTG TGGGAGGTGC TGATGCTCTG 2600  
 10 TAGGGCCCAG CCCTTTGGGC AGCTCACCGA CGAGCAGGTC ATCGAGAACG 2650  
 CGGGGGAGTT CTTCCGGGAC CAGGGCCGGC AGGTGTACCT GTCCCGGCCG 2700  
 15 CCTGCCTGCC CGCAGGGCCT ATATGAGCTG ATGCTTCGGT GCTGGAGCCG 2750  
 GGAGTCTGAG CAGCGACCAC CCTTTTCCCA GCTGCATCGG TTCCTGGCAG 2800  
 20 AGGATGCACT CAACACGGTG TGAATCACAC ATCCAGCTGC CCCTCCCTCA 2850  
 GGGAGTGATC CAGGGGAAGC CAGTGACACT AAAACAAGAG GACACAATGG 2900  
 CACCTCTGCC CTTCCCCTCC CGACAGCCCA TCACCTCTAA TAGAGGCAGT 2950  
 30 GAGACTGCAG AAGCCCCTGT CGCCCACCCA GCTGGTCCTG TGGATGGGAT 3000  
 CCTCTCCACC CTCCTCTAGC CATCCCTTGG GGAAGGGTGG GGAGAAATAT 3050  
 35 AGGATAGACA CTGGACATGG CCCATTGGAG CACCTGGGCC CCACTGGACA 3100  
 AACTGATTC CTGGAGAGGT GGCTGCGCCC CCAGCTTCTC TCTCCCTGTC 3150  
 ACACACTGGA CCCCACTGGC TGAGAATCTG GGGGTGAGGA GGACAAGAAG 3200  
 45 GAGAGGAAAA TGTTTCCTTG TGCCTGCTCC TGTACTTGTC CTCAGCTTGG 3250  
 GCTTCTTCCT CCTCCATCAC CTGAAACACT GGACCTGGGG GTAGCCCCGC 3300  
 50 CCCAGCCCTC AGTCACCCCC ACTTCCCACC TGCAGTCTTG TAGCTAGAAC 3350

TTCTCTAAGC CTATACGTTT CTGTGGAGTA AATATTGGGA TTGGGGGGAA 3400

5 AGAGGGGAGCA ACGGCCCATATA GCCTTGGGGT TGGACATCTC TAGTGTAGCT 3450

GCCACATTGA TTTTCTATA ATCACTTGGG GTTGTACAT TTTTGGGGGG 3500

10 AGAGACACAG ATTTTACAC TAATATATGG ACCTAGCTTG AGGCAATTTT 3550

15 AATCCCCTGC ACTAGGCAGG TAATAATAAA GGTGAGTTT TCCACAAAAA 3600

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 3637

20 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 913 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 Met Gly Pro Glu Ala Leu Ser Ser Leu Leu Leu Leu Leu Val  
1 5 10 15

Ala Ser Gly <sup>19</sup>(Asp) Ala Asp Met Lys Gly His Phe Asp Pro Ala Lys  
20 25 30

35 Cys Arg Tyr Ala Leu Gly Met Gln Asp Arg Thr Ile Pro Asp Ser  
35 40 45

40 Asp Ile Ser Ala Ser Ser Ser Trp Ser Asp Ser Thr Ala Ala Arg  
50 55 60

His Ser Arg Leu Glu Ser Ser Asp Gly Asp Gly Ala Trp Cys Pro  
65 70 75

45 Ala Gly Ser Val Phe Pro Lys Glu Glu Glu Tyr Leu Gln Val Asp  
80 85 90

Leu Gln Arg Leu His Leu Val Ala Leu Val Gly Thr Gln Gly Arg  
95 100 105

50 His Ala Gly Gly Leu Gly Lys Glu Phe Ser Arg Ser Tyr Arg Leu  
110 115 120

	Arg	Tyr	Ser	Arg	Asp 125	Gly	Arg	Arg	Trp	Met 130	Gly	Trp	Lys	Asp	Arg 135
5	Trp	Gly	Gln	Glu	Val 140	Ile	Ser	Gly	Asn	Glu 145	Asp	Pro	Glu	Gly	Val 150
	Val	Leu	Lys	Asp	Leu 155	Gly	Pro	Pro	Met	Val 160	Ala	Arg	Leu	Val	Arg 165
10	Phe	Tyr	Pro	Arg	Ala 170	Asp	Arg	Val	Met	Ser 175	Val	Cys	Leu	Arg	Val 180
	Glu	Leu	Tyr	Gly	Cys 185	Leu	Trp	Arg	Asp	Gly 190	Leu	Leu	Ser	Tyr	Thr 195
15	Ala	Pro	Val	Gly	Gln 200	Thr	Met	Tyr	Leu	Ser 205	Glu	Ala	Val	Tyr	Leu 210
	Asn	Asp	Ser	Thr	Tyr 215	Asp	Gly	His	Thr	Val 220	Gly	Gly	Leu	Gln	Tyr 225
20	Gly	Gly	Leu	Gly	Gln 230	Leu	Ala	Asp	Gly	Val 235	Val	Gly	Leu	Asp	Asp 240
25	Phe	Arg	Lys	Ser	Gln 245	Glu	Leu	Arg	Val	Trp 250	Pro	Gly	Tyr	Asp	Tyr 255
	Val	Gly	Trp	Ser	Asn 260	His	Ser	Phe	Ser	Ser 265	Gly	Tyr	Val	Glu	Met 270
30	Glu	Phe	Glu	Phe	Asp 275	Arg	Leu	Arg	Ala	Phe 280	Gln	Ala	Met	Gln	Val 285
	His	Cys	Asn	Asn	Met 290	His	Thr	Leu	Gly	Ala 295	Arg	Leu	Pro	Gly	Gly 300
35	Val	Glu	Cys	Arg	Phe 305	Arg	Arg	Gly	Pro	Ala 310	Met	Ala	Trp	Glu	Gly 315
40	Glu	Pro	Met	Arg	His 320	Asn	Leu	Gly	Gly	Asn 325	Leu	Gly	Asp	Pro	Arg 330
	Ala	Arg	Ala	Val	Ser 335	Val	Pro	Leu	Gly	Gly 340	Arg	Val	Ala	Arg	Phe 345
45	Leu	Gln	Cys	Arg	Phe 350	Leu	Phe	Ala	Gly	Pro 355	Trp	Leu	Leu	Phe	Ser 360
50	Glu	Ile	Ser	Phe	Ile 365	Ser	Asp	Val	Val	Asn 370	Asn	Ser	Ser	Pro	Ala 375

	Leu Gly Gly Thr	Phe 380	Pro Pro Ala Pro	Trp 385	Trp Pro Pro Gly	Pro 390
5	Pro Pro Thr Asn	Phe 395	Ser Ser Leu Glu	Leu 400	Glu Pro Arg Gly	Gln 405
	Gln Pro Val Ala	Lys 410	Pro Glu Gly Ser	Pro 415	Thr <u>Ala</u> Ile Leu	Ile 420
10	Gly Cys Leu Val	Ala 425	Ile Ile Leu Leu	Leu 430	Leu Leu Ile Ile	Ala 435
	Leu Met Leu Trp	Arg 440	Leu His Trp Arg	Arg 445	Leu Leu Ser Lys	Ala 450
15	Glu Arg Arg Val	Leu 455	Glu Glu Glu Leu	Thr 460	Val His Leu Ser	Val 465
20	Pro Gly Asp Thr	Ile 470	Leu Ile Asn Asn	Arg 475	Pro Gly Pro Arg	Glu 480
	Pro Pro Pro Tyr	Gln 485	Glu Pro Arg Pro	Arg 490	Gly Asn Pro Pro	His 495
25	Ser Ala Pro Cys	Val 500	Pro Asn Gly Ser	Ala 505	Leu Leu Leu Ser	Asn 510
	Pro Ala Tyr Arg	Leu 515	Leu Leu Ala Thr	Tyr 520	Ala Arg Pro Pro	Arg 525
30	Gly Pro Gly Pro	Pro 530	Thr Pro Ala Trp	Ala 535	Lys Pro Thr Asn	Thr 540
35	Gln Ala Tyr Ser	Gly 545	Asp Tyr Met Glu	Pro 550	Glu Lys Pro Gly	Ala 555
	Pro Leu Leu Pro	Pro 560	Pro Pro Gln Asn	Ser 565	Val Pro His Tyr	Ala 570
40	Glu Ala Asp Ile	Val 575	Thr Leu Gln Gly	Val 580	Thr Gly Gly Asn	Thr 585
	Tyr Ala Val Pro	Ala 590	Leu Pro Pro Gly	Ala 595	Val Gly Asp Gly	Pro 600
45	Pro Arg Val Asp	Phe 605	Pro Arg Ser Arg	Leu 610	Arg Phe Lys Glu	Lys 615
50	Leu Gly Glu Gly	Gln 620	Phe Gly Glu Val	His 625	Leu Cys Glu Val	Asp 630



	Ser	Pro	Gln	Asp	Leu	Val	Ser	Leu	Asp	Phe	Pro	Leu	Asn	Val	Arg	
					635					640					645	
5	Lys	Gly	His	Pro	Leu	Leu	Val	Ala	Val	Lys	Ile	Leu	Arg	Pro	Asp	
					650					655					660	
	Ala	Thr	Lys	Asn	Ala	Arg	Asn	Asp	Phe	Leu	Lys	Glu	Val	Lys	Ile	
					665					670					675	
10	Met	Ser	Arg	Leu	Lys	Asp	Pro	Asn	Ile	Ile	Arg	Leu	Leu	Gly	Val	
					680					685					690	
	Cys	Val	Gln	Asp	Asp	Pro	Leu	Cys	Met	Ile	Thr	Asp	Tyr	Met	Glu	
					695					700					705	
15	Asn	Gly	Asp	Leu	Asn	Gln	Phe	Leu	Ser	Ala	His	Gln	Leu	Glu	Asp	
					710					715					720	
	Lys	Ala	Ala	Glu	Gly	Ala	Pro	Gly	Asp	Gly	Gln	Ala	Ala	Gln	Gly	
20					725					730					735	
	Pro	Thr	Ile	Ser	Tyr	Pro	Met	Leu	Leu	His	Val	Ala	Ala	Gln	Ile	
					740					745					750	
25	Ala	Ser	Gly	Met	Arg	Tyr	Leu	Ala	Thr	Leu	Asn	Phe	Val	His	Arg	
					755					760					765	
	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Phe	Thr	Ile	
30					770					775					780	
	Lys	Ile	Ala	Asp	Phe	Gly	Met	Ser	Arg	Asn	Leu	Tyr	Ala	Gly	Asp	
					785					790					795	
	Tyr	Tyr	Arg	Val	Gln	Gly	Arg	Ala	Val	Leu	Pro	Ile	Arg	Trp	Met	
35					800					805					810	
	Ala	Trp	Glu	Cys	Ile	Leu	Met	Gly	Lys	Phe	Thr	Thr	Ala	Ser	Asp	
					815					820					825	
40	Val	Trp	Ala	Phe	Gly	Val	Thr	Leu	Trp	Glu	Val	Leu	Met	Leu	Cys	
					830					835					840	
	Arg	Ala	Gln	Pro	Phe	Gly	Gln	Leu	Thr	Asp	Glu	Gln	Val	Ile	Glu	
					845					850					855	
45	Asn	Ala	Gly	Glu	Phe	Phe	Arg	Asp	Gln	Gly	Arg	Gln	Val	Tyr	Leu	
					860					865					870	
	Ser	Arg	Pro	Pro	Ala	Cys	Pro	Gln	Gly	Leu	Tyr	Glu	Leu	Met	Leu	
50					875					880					885	

Arg	Cys	Trp	Ser	Arg	Glu	Ser	Glu	Gln	Arg	Pro	Pro	Phe	Ser	Gln
				890					895					900
Leu	His	Arg	Phe	Leu	Ala	Glu	Asp	Ala	Leu	Asn	Thr	Val		
				905					910			913		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GCAGGTCTGA AGCTCATGGG AGCCCCGGTG AAGCTGACAG TGTCTCAGGG 50
GCAGCCGGTG AAGCTCAACT GCAGTGTGGA GGGGATGGAG GAGCCTGACA 100
TCCAGTGGGT GAAGGATGGG GCTGTGGTCC AGAACTTGA CCAGTTGTAC 150
ATCCCAGTCA GCGAGCAGCA CTGGATCGGC TTCCTCAGCC TGAAGTCAGT 200
GGAGCGCTCT GACGCCGGCC GGTACTGGTG CCAGGTGGAG GATGGGGGTG 250
AAACCGAGAT CTCCCAGCCA GTGTGGCTCA CGGTAGAAGG TGTGCCATTT 300
TTCACAGTGG AGCCAAAAGA TCTGGCAGTG CCACCCAATG CCCCTTTCCA 350
ACTGTCTTGT GAGGCTGTGG GTCCCCCTGA ACCTGTTACC ATTGTCTGGT 400
GGAGAGGAAC TACGAAGATC GGGGGACCCG CTCCCTCTCC ATCTGTTTTA 450
AATGTAACAG GGGTGACCCA GAGCACCATG TTTTCCTGTG AAGCTCACAA 500
CCTAAAAGGC CTGGCCTCTT CTCGCACAGC CACTGTTCAC CTTCAAGCAC 550
TGCCTGCAGC CCCCTTCAAC ATCACCGTGA CAAAGCTTTC CAGCAGCAAC 600

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GCTAGTGTGG CCTGGATGCC AGGTGCTGAT GGCCGAGCTC TGCTACAGTC 650

CTGTACAGTT CAGGTGACAC AGGCCCCAGG AGGCTGGGAA GTCCTGGCTG 700

TTGTGGTCCC TGTGCCCCCC TTTACCTGCC TGCTCCGGGA CCTGGTGCCT 750

GCCACCAACT ACAGCCTCAG GGTGCGCTGT GCCAATGCCT TGGGGCCCTC 800

TCCCTATGCT GACTGGGTGC CCTTTCAGAC CAAGGGTCTA GCCCCAGCCA 850

GCGCTCCCCA AAACCTCCAT GCCATCCGCA CAGATTCAGG CCTCATCTTG 900

GAGTGGGAAG AAGTGATCCC CGAGGCCCTT TTGGAAGGCC CCCTGGGACC 950

CTACAAACTG TCCTGGGTTC AAGACAATGG AACCCAGGAT GAGCTGACAG 1000

TGGAGGGGAC CAGGGCCAAT TTGACAGGCT GGGATCCCCA AAAGGACCTG 1050

ATCGTACGTG TGTGCGTCTC CAATGCAGTT GGCTGTGGAC CCTGGAGTCA 1100

GCCACTGGTG GTCTCTTCTC ATGACCGTGC AGGCCAGCAG GGCCCTCCTC 1150

ACAGCCGCAC ATCC 1164

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Gly Leu Lys Leu Met Gly Ala Pro Val Lys Leu Thr Val Ser  
1 5 10 15

Gln Gly Gln Pro Val Lys Leu Asn Cys Ser Val Glu Gly Met Glu  
20 25 30

	Glu	Pro	Asp	Ile	Gln	Trp	Val	Lys	Asp	Gly	Ala	Val	Val	Gln	Asn	
					35					40					45	
5	Leu	Asp	Gln	Leu	Tyr	Ile	Pro	Val	Ser	Glu	Gln	His	Trp	Ile	Gly	
					50					55					60	
	Phe	Leu	Ser	Leu	Lys	Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	
					65					70					75	
10	Trp	Cys	Gln	Val	Glu	Asp	Gly	Gly	Glu	Thr	Glu	Ile	Ser	Gln	Pro	
					80					85					90	
	Val	Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	
					95					100					105	
15	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser	Cys	
					110					115					120	
	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Val	Trp	Trp	Arg	
20					125					130					135	
	Gly	Thr	Thr	Lys	Ile	Gly	Gly	Pro	Ala	Pro	Ser	Pro	Ser	Val	Leu	
					140					145					150	
25	Asn	Val	Thr	Gly	Val	Thr	Gln	Ser	Thr	Met	Phe	Ser	Cys	Glu	Ala	
					155					160					165	
	His	Asn	Leu	Lys	Gly	Leu	Ala	Ser	Ser	Arg	Thr	Ala	Thr	Val	His	
30					170					175					180	
	Leu	Gln	Ala	Leu	Pro	Ala	Ala	Pro	Phe	Asn	Ile	Thr	Val	Thr	Lys	
					185					190					195	
	Leu	Ser	Ser	Ser	Asn	Ala	Ser	Val	Ala	Trp	Met	Pro	Gly	Ala	Asp	
35					200					205					210	
	Gly	Arg	Ala	Leu	Leu	Gln	Ser	Cys	Thr	Val	Gln	Val	Thr	Gln	Ala	
					215					220					225	
40	Pro	Gly	Gly	Trp	Glu	Val	Leu	Ala	Val	Val	Val	Pro	Val	Pro	Pro	
					230					235					240	
	Phe	Thr	Cys	Leu	Leu	Arg	Asp	Leu	Val	Pro	Ala	Thr	Asn	Tyr	Ser	
					245					250					255	
45	Leu	Arg	Val	Arg	Cys	Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Ala	
					260					265					270	
	Asp	Trp	Val	Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Ser	Ala	
50					275					280					285	

	Pro	Gln	Asn	Leu	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	
					290					295					300	
5	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Ala	Pro	Leu	Glu	Gly	Pro	Leu	
					305					310					315	
	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Asp	Asn	Gly	Thr	Gln	Asp	
					320					325					330	
10	Glu	Leu	Thr	Val	Glu	Gly	Thr	Arg	Ala	Asn	Leu	Thr	Gly	Trp	Asp	
					335					340					345	
	Pro	Gln	Lys	Asp	Leu	Ile	Val	Arg	Val	Cys	Val	Ser	Asn	Ala	Val	
15					350					355					360	
	Gly	Cys	Gly	Pro	Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	
					365					370					375	
20	Arg	Ala	Gly	Gln	Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser			
					380					385					388	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1197 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATGCTGACA TGAAGGGACA TTTTGATCCT GCCAAGTGCC GCTATGCCCT 50

GGGCATGCAG GACCGGACCA TCCCAGACAG TGACATCTCT GCTTCCAGCT 100

CCTGGTCAGA TTCCACTGCC GCCCGCCACA GCAGGTTGGA GAGCAGTGAC 150

GGGGATGGGG CCTGGTGCCC CGCAGGGTCG GTGTTTCCCA AGGAGGAGGA 200

GTACTTGCAG GTGGATCTAC AACGACTGCA CCTGGTGGCT CTGGTGGGCA 250

CCCAGGGACG GCATGCCGGG GGCCTGGGCA AGGAGTTCTC CCGGAGCTAC 300

CGGCTGCGTT ACTCCCGGGA TGGTCGCCGC TGGATGGGCT GGAAGGACCG 350

CTGGGGTCAG GAGGTGATCT CAGGCAATGA GGACCCTGAG GGAGTGGTGC 400

5 TGAAGGACCT TGGGCCCCC ATGGTTGCCC GACTGGTTCG CTTCTACCCC 450

CGGGCTGACC GGGTCATGAG CGTCTGTCTG CGGGTAGAGC TCTATGGCTG 500

10 CCTCTGGAGG GATGGACTCC TGTCTTACAC CGCCCCTGTG GGGCAGACAA 550

TGTATTTATC TGAGGCCGTG TACCTCAACG ACTCCACCTA TGACGGACAT 600

15 ACCGTGGGCG GACTGCAGTA TGGGGGTCTG GGCCAGCTGG CAGATGGTGT 650

20 GGTGGGGCTG GATGACTTTA GGAAGAGTCA GGAGCTGCGG GTCTGGCCAG 700

GCTATGACTA TGTGGGATGG AGCAACCACA GCTTCTCCAG TGGCTATGTG 750

25 GAGATGGAGT TTGAGTTTGA CCGGCTGAGG GCCTTCCAGG CTATGCAGGT 800

CCACTGTAAC AACATGCACA CGCTGGGAGC CCGTCTGCCT GGCGGGGTGG 850

30 AATGTCGCTT CCGGCGTGGC CCTGCCATGG CCTGGGAGGG GGAGCCCATG 900

35 CGCCACAACC TAGGGGGCAA CCTGGGGGAC CCCAGAGCCC GGGCTGTCTC 950

AGTGCCCCTT GGC GGCGCCGTG TGGCTCGCTT TCTGCAGTGC CGCTTCCTCT 1000

40 TTGCGGGGCC CTGGTTACTC TTCAGCGAAA TCTCCTTCAT CTCTGATGTG 1050

GTGAACAATT CCTCTCCGGC ACTGGGAGGC ACCTTCCCGC CAGCCCCCTG 1100

45 GTGGCCGCCT GGCCACCTC CCACCAACTT CAGCAGCTTG GAGCTGGAGC 1150

50 CCAGAGGCCA GCAGCCCGTG GCCAAGCCCG AGGGGAGCCC GACCGCC 1197

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10	Asp	Ala	Asp	Met	Lys	Gly	His	Phe	Asp	Pro	Ala	Lys	Cys	Arg	Tyr
	1				5					10					15
	Ala	Leu	Gly	Met	Gln	Asp	Arg	Thr	Ile	Pro	Asp	Ser	Asp	Ile	Ser
					20					25					30
15	Ala	Ser	Ser	Ser	Trp	Ser	Asp	Ser	Thr	Ala	Ala	Arg	His	Ser	Arg
					35					40					45
	Leu	Glu	Ser	Ser	Asp	Gly	Asp	Gly	Ala	Trp	Cys	Pro	Ala	Gly	Ser
20					50					55					60
	Val	Phe	Pro	Lys	Glu	Glu	Glu	Tyr	Leu	Gln	Val	Asp	Leu	Gln	Arg
					65					70					75
25	Leu	His	Leu	Val	Ala	Leu	Val	Gly	Thr	Gln	Gly	Arg	His	Ala	Gly
					80					85					90
	Gly	Leu	Gly	Lys	Glu	Phe	Ser	Arg	Ser	Tyr	Arg	Leu	Arg	Tyr	Ser
					95					100					105
30	Arg	Asp	Gly	Arg	Arg	Trp	Met	Gly	Trp	Lys	Asp	Arg	Trp	Gly	Gln
					110					115					120
	Glu	Val	Ile	Ser	Gly	Asn	Glu	Asp	Pro	Glu	Gly	Val	Val	Leu	Lys
35					125					130					135
	Asp	Leu	Gly	Pro	Pro	Met	Val	Ala	Arg	Leu	Val	Arg	Phe	Tyr	Pro
					140					145					150
40	Arg	Ala	Asp	Arg	Val	Met	Ser	Val	Cys	Leu	Arg	Val	Glu	Leu	Tyr
					155					160					165
	Gly	Cys	Leu	Trp	Arg	Asp	Gly	Leu	Leu	Ser	Tyr	Thr	Ala	Pro	Val
					170					175					180
45	Gly	Gln	Thr	Met	Tyr	Leu	Ser	Glu	Ala	Val	Tyr	Leu	Asn	Asp	Ser
					185					190					195
	Thr	Tyr	Asp	Gly	His	Thr	Val	Gly	Gly	Leu	Gln	Tyr	Gly	Gly	Leu
50					200					205					210

	Gly	Gln	Leu	Ala	Asp	Gly	Val	Val	Gly	Leu	Asp	Asp	Phe	Arg	Lys	
					215					220						225
5	Ser	Gln	Glu	Leu	Arg	Val	Trp	Pro	Gly	Tyr	Asp	Tyr	Val	Gly	Trp	
					230					235						240
	Ser	Asn	His	Ser	Phe	Ser	Ser	Gly	Tyr	Val	Glu	Met	Glu	Phe	Glu	
					245					250						255
10	Phe	Asp	Arg	Leu	Arg	Ala	Phe	Gln	Ala	Met	Gln	Val	His	Cys	Asn	
					260					265						270
	Asn	Met	His	Thr	Leu	Gly	Ala	Arg	Leu	Pro	Gly	Gly	Val	Glu	Cys	
					275					280						285
15	Arg	Phe	Arg	Arg	Gly	Pro	Ala	Met	Ala	Trp	Glu	Gly	Glu	Pro	Met	
					290					295						300
	Arg	His	Asn	Leu	Gly	Gly	Asn	Leu	Gly	Asp	Pro	Arg	Ala	Arg	Ala	
20					305					310						315
	Val	Ser	Val	Pro	Leu	Gly	Gly	Arg	Val	Ala	Arg	Phe	Leu	Gln	Cys	
					320					325						330
25	Arg	Phe	Leu	Phe	Ala	Gly	Pro	Trp	Leu	Leu	Phe	Ser	Glu	Ile	Ser	
					335					340						345
	Phe	Ile	Ser	Asp	Val	Val	Asn	Asn	Ser	Ser	Pro	Ala	Leu	Gly	Gly	
					350					355						360
30	Thr	Phe	Pro	Pro	Ala	Pro	Trp	Trp	Pro	Pro	Gly	Pro	Pro	Pro	Thr	
					365					370						375
	Asn	Phe	Ser	Ser	Leu	Glu	Leu	Glu	Pro	Arg	Gly	Gln	Gln	Pro	Val	
35					380					385						390
	Ala	Lys	Pro	Glu	Gly	Ser	Pro	Thr	Ala							
					395					399						

40 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 3785 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

50 CCTCCGCCAC CCTCCTCTCA GCGCTCGCGG GCCGGGCCCCG GCATGGTGCG 50



CGTCGCCGCC GATGGCGCTG AGGCGGAGCA TGGGGTGGCC GGGGCTCCGG 100

CCGCTGCTGC TGGCGGGACT GGCTTCTCTG CTGCTCCCCG GGTCTGCGGC 150

CGCAGGCCTG AAGCTCATGG GCGCCCCAGT GAAGATGACC GTGTCTCAGG 200

GGCAGCCAGT GAAGCTCAAC TGCAGCGTGG AGGGGATGGA GGACCCTGAC 250

ATCCTACTGGA TGAAGGATGG CACCGTGGTC CAGAATGCAA GCCAGGTGTC 300

CATCTCCATC AGCGAGCACA GCTGGATTGG CTTACTCAGC CTAAAGTCAG 350

TGGAGCGGTC TGATGCTGGC CTGTACTGGT GCCAGGTGAA GGATGGGGAG 400

GAAACCAAGA TCTCTCAGTC AGTATGGCTC ACTGTCGAAG GTGTGCCATT 450

CTTCACAGTG GAACCAAAAG ATCTGGCGGT GCCACCCAAT GCCCCTTTTC 500

AGCTGTCTTG TGAGGCTGTG GGTCTCTCCAG AACCCGTAAC CATTTACTGG 550

TGGAGAGGAC TACTAAGGT TGGGGGACCT GCTCCCTCTC CCTCTGTTTT 600

AAATGTGACA GGAGTGACCC AGCGCACAGA GTTTTCTTGT GAAGCCCGCA 650

ACATAAAAGG CCTGGCCACT TCCCGACCAG CCATTGTTCTG CCTTCAAGCA 700

CCGCCTGCAG CTCCTTTCAA CACCACAGTA ACAACGATCT CCAGCTACAA 750

CGCTAGCGTG GCCTGGGTGC CAGGTGCTGA CGGCCTAGCT CTGCTGCATT 800

CCTGTACTGT ACAGGTGGCA CACGCCCCAG GAGAATGGGA GGCCCTTGCT 850

GTTGTGGTTC CTGTGCCACC TTTTACCTGC CTGCTTCGGA ACTTGGCCCC 900

TGCCACCAAC TACAGCCTTA GGGTGCGCTG TGCCAATGCC TTGGGCCCTT 950

CTCCCTACGG CGACTGGGTG CCCTTTCAGA CAAAGGGCCT AGCGCCAGCC 1000  
 5 AGAGCTCCTC AGAATTTCCA TGCCATTTCGT ACCGACTCAG GCCTTATCCT 1050  
 GGAATGGGAA GAAGTGATTC CTGAAGACCC TGGGGAAGGC CCCCTAGGAC 1100  
 10 CTTATAAGCT GTCCTGGGTC CAAGAAAATG GAACCCAGGA TGAGCTGATG 1150  
 GTGGAAGGGA CCAGGGCCAA TCTGACCGAC TGGGATCCCC AGAAGGACCT 1200  
 15 GATTTTTCGT GTGTGTGCCT CCAATGCAAT TGGTGATGGG CCCTGGAGTC 1250  
 20 AGCCACTGGT GGTGTCTTCT CATGACCATG CAGGGAGGCA GGGCCCTCCC 1300  
 CACAGCCGCA CATCCTGGGT GCCTGTGGTC CTGGGCGTGC TCACCGCCCT 1350  
 25 GATCACAGCT GCTGCCTTGG CCCTCATCCT GCTTCGGAAG AGACGCAAGG 1400  
 AGACGCGTTT CGGGCAAGCC TTTGACAGTG TCATGGCCCG AGGGGAGCCA 1450  
 30 GCTGTACACT TCCGGGCAGC CCGATCTTTC AATCGAGAAA GGCCTGAACG 1500  
 35 CATTGAGGCC ACATTGGATA GCCTGGGCAT CAGCGATGAA TTGAAGGAAA 1550  
 AGCTGGAGGA TGTCTTCATT CCAGAGCAGC AGTTCACCCT CGGTCGGATG 1600  
 40 TTGGGCAAAG GAGAGTTTGG ATCAGTGCGG GAAGCCCAGC TAAAGCAGGA 1650  
 45 AGATGGCTCC TTCGTGAAAG TGGCAGTGAA GATGCTGAAA GCTGACATCA 1700  
 TTGCCTCAAG CGACATAGAA GAGTTCCTCC GGGAAGCAGC TTGCATGAAG 1750  
 50 GAGTTTGACC ATCCACACGT GGCCAAGCTT GTTGGGGTGA GCCTCCGGAG 1800

CAGGGCTAAA GGTCGTCTCC CCATTCCCAT GGTCATCCTG CCCTTCATGA 1850  
 AACATGGAGA CTTGCACGCC TTTCTGCTCG CCTCCCGAAT CGGGGAGAAC 1900  
 5 CCTTTTAACC TGCCCCTGCA GACCCTGGTC CGGTTCATGG TGGACATTGC 1950  
 CTGTGGCATG GAGTACCTGA GCTCCCGGAA CTTTCATCCAC CGAGACCTAG 2000  
 CAGCTCGGAA TTGCATGCTG GCCGAGGACA TGACAGTGTG TGTGGCTGAT 2050  
 15 TTTGGACTCT CTCGGAAAAT CTATAGCGGG GACTATTATC GTCAGGGCTG 2100  
 TGCCTCCAAA TTGCCCCGTCA AGTGGCTGGC CCTGGAGAGC TTGGCTGACA 2150  
 20 ACTTGTATAC TGTACACAGT GATGTGTGGG CCTTCGGGGT GACCATGTGG 2200  
 GAGATCATGA CTCGTGGGCA GACGCCATAT GCTGGCATTG AAAATGCTGA 2250  
 GATTTACAAC TACCTCATCG GCGGGAACCG CCTGAAGCAG CCTCCGGAGT 2300  
 30 GCATGGAGGA AGTGTATGAT CTCATGTACC AGTGCTGGAG CGCCGACCCC 2350  
 AAGCAGCGCC CAAGCTTCAC GTGTCTGCGA ATGGAAGTGG AGAACATTCT 2400  
 35 GGGCCACCTG TCTGTGCTGT CCACCAGCCA GGACCCCTTG TACATCAACA 2450  
 TTGAGAGAGC TGAGCAGCCT ACTGAGAGTG GCAGCCCTGA GCTGCACTGT 2500  
 GGAGAGCGAT CCAGCAGCGA GGCAGGGGAC GGCAGTGGCG TGGGGGCAGT 2550  
 45 AGGTGGCATC CCCAGTGACT CTCGGTACAT CTTAGCCCC GGAGGGCTAT 2600  
 CCGAGTCACC AGGGCAGCTG GAGCAGCAGC CAGAAAGCCC CCTCAATGAG 2650  
 50 AACCAGAGGC TGTGTGTGCT GCAGCAAGGG CTACTGCCTC ACAGTAGCTG 2700

TTAACCTCA GGCAGAGGAA AGTTGGGGCC CCTGGCTCTG CTGACCGCTG 2750

5 CGCTGCCTGA CTAGGCCAG TCTGATCACA GCCCAGGCAG CAAGGTATGG 2800

AGGCTCCTGT GGTAGCCCTC CCAAGCTGTG TGGCGCCTGG ACGGACCAAA 2850

10 TTGCCCAATC CCAGTTCTTC CTGCAGCCGC TCTGGCCAGC CTGGCATCAG 2900

TTCAGGCCTT GGCTTAGAGG AGGTGAGCCA GAGCTGGTTG CCTGAATGCA 2950

15 GGCAGCTGGC AGGAGGGGAG GGTGGCTATG TTTCCATGGG TACCATGGGT 3000

20 GTGGATGGCA GTAAGGGAGG GTAGCAACAG CCTGTGGGCC CCTACCCTCC 3050

TGGCTGAGCT GCTCCTACTT TAGTGCATGC TTGGAGCCGC CTGCAGCCTG 3100

25 GAACTCAGCA CTGCCCACCA CACTTGGGCC GAAATGCCAG GTTTGCCCCT 3150

CTTAAGTCAC AAAGAGATGT CCATGTATTG TTCCCTTTTA GGTGATGATT 3200

30 AGGAAGGGAT TGGCACACTT GGTCCCTAA GCCCTATGGC AGGAAATGGT 3250

35 GGGATATTCT CAGGTCTGAA TCCTCATCAT CTTCTGATT CCCACCTG 3300

CAAAGGCCTG GAACTGGCTG TGGGGCTCTG ACGCATGCTG AAGGACAAAA 3350

40 GGTACAGAG ATCCGACTTC AAAAGGCAGG GTCTGAGTCT GGCAGGTGGA 3400

GAGGTGCTAA GGGGCTGGCC CAGGAGTCAG GCATTTCAGG ACCCTCCAA 3450

45 GCTTCTACAG TCTGTCTGAG CATGCTACCA AGCCCCAGA TACCCAAAA 3500

50 CTAACAGAGG CAGTTTTGTC TGAGCCCAGC CCTCCACAT GATGACCCTT 3550

AGGTCTACCC TCCTCTCTAA ATGGACATCC TCGTTTGTCC CAAGTCTCCA 3600

GAGAGACTAC TGATGGCTGA TGTGGGTAAG AAAAGTTCCA GGAACCAGGG 3650

CTGGGGTGGA ACCAGGGCTG GGGTCGAGGC AGGCTCTTGG GCAGGCTCTT 3700

GCTGTTAGGA ACATTTCTAA GCTATTAAGT TGCTGTTTCA AAACAAATAA 3750

AATTGAAACA TAAAGAATCA AAAAAAAAAA AAAAA 3785

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 880 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Leu	Arg	Arg	Ser	Met	Gly	Trp	Pro	Gly	Leu	Arg	Pro	Leu
1				5					10					15
Leu	Leu	Ala	Gly	Leu	Ala	Ser	Leu	Leu	Leu	Pro	Gly	Ser	Ala	Ala
				20					25					30
Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser
				35					40					45
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly	Met	Glu
				50					55					60
Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr	Val	Val	Gln	Asn
				65					70					75
Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser	Glu	His	Ser	Trp	Ile	Gly
				80					85					90
Leu	Leu	Ser	Leu	Lys	Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr
				95					100					105
Trp	Cys	Gln	Val	Lys	Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser
				110					115					120
Val	Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro
				125					130					135

	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser	Cys	
					140					145					150	
5	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr	Trp	Trp	Arg	
					155					160					165	
	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro	Ser	Pro	Ser	Val	Leu	
					170					175					180	
10	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg	Thr	Glu	Phe	Ser	Cys	Glu	Ala	
					185					190					195	
	Arg	Asn	Ile	Lys	Gly	Leu	Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	
					200					205					210	
15	Leu	Gln	Ala	Pro	Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	
					215					220					225	
	Ile	Ser	Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp	
20					230					235					240	
	Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala	His	Ala	
					245					250					255	
25	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val	Pro	Val	Pro	Pro	
					260					265					270	
	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala	Pro	Ala	Thr	Asn	Tyr	Ser	
					275					280					285	
30	Leu	Arg	Val	Arg	Cys	Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	
					290					295					300	
	Asp	Trp	Val	Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	
35					305					310					315	
	Pro	Gln	Asn	Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	
					320					325					330	
40	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro	Leu	
					335					340					345	
	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly	Thr	Gln	Asp	
					350					355					360	
45	Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn	Leu	Thr	Asp	Trp	Asp	
					365					370					375	
	Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg	Val	Cys	Ala	Ser	Asn	Ala	Ile	
50					380					385					390	

	Gly	Asp	Gly	Pro	Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp	
					395					400					405	
5	His	Ala	Gly	Arg	Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser	Trp	Val	
					410					415					420	
	Pro	Val	Val	Leu	Gly	Val	Leu	Thr	Ala	Leu	Ile	Thr	Ala	Ala	Ala	
					425					430					435	
10	Leu	Ala	Leu	Ile	Leu	Leu	Arg	Lys	Arg	Arg	Lys	Glu	Thr	Arg	Phe	
					440					445					450	
	Gly	Gln	Ala	Phe	Asp	Ser	Val	Met	Ala	Arg	Gly	Glu	Pro	Ala	Val	
					455					460					465	
15	His	Phe	Arg	Ala	Ala	Arg	Ser	Phe	Asn	Arg	Glu	Arg	Pro	Glu	Arg	
					470					475					480	
20	Ile	Glu	Ala	Thr	Leu	Asp	Ser	Leu	Gly	Ile	Ser	Asp	Glu	Leu	Lys	
					485					490					495	
	Glu	Lys	Leu	Glu	Asp	Val	Leu	Ile	Pro	Glu	Gln	Gln	Phe	Thr	Leu	
					500					505					510	
25	Gly	Arg	Met	Leu	Gly	Lys	Gly	Glu	Phe	Gly	Ser	Val	Arg	Glu	Ala	
					515					520					525	
	Gln	Leu	Lys	Gln	Glu	Asp	Gly	Ser	Phe	Val	Lys	Val	Ala	Val	Lys	
					530					535					540	
30	Met	Leu	Lys	Ala	Asp	Ile	Ile	Ala	Ser	Ser	Asp	Ile	Glu	Glu	Phe	
					545					550					555	
35	Leu	Arg	Glu	Ala	Ala	Cys	Met	Lys	Glu	Phe	Asp	His	Pro	His	Val	
					560					565					570	
	Ala	Lys	Leu	Val	Gly	Val	Ser	Leu	Arg	Ser	Arg	Ala	Lys	Gly	Arg	
					575					580					585	
40	Leu	Pro	Ile	Pro	Met	Val	Ile	Leu	Pro	Phe	Met	Lys	His	Gly	Asp	
					590					595					600	
	Leu	His	Ala	Phe	Leu	Leu	Ala	Ser	Arg	Ile	Gly	Glu	Asn	Pro	Phe	
					605					610					615	
45	Asn	Leu	Pro	Leu	Gln	Thr	Leu	Val	Arg	Phe	Met	Val	Asp	Ile	Ala	
					620					625					630	
50	Cys	Gly	Met	Glu	Tyr	Leu	Ser	Ser	Arg	Asn	Phe	Ile	His	Arg	Asp	
					635					640					645	

	Leu	Ala	Ala	Arg	Asn	Cys	Met	Leu	Ala	Glu	Asp	Met	Thr	Val	Cys	650	655	660
5	Val	Ala	Asp	Phe	Gly	Leu	Ser	Arg	Lys	Ile	Tyr	Ser	Gly	Asp	Tyr	665	670	675
	Tyr	Arg	Gln	Gly	Cys	Ala	Ser	Lys	Leu	Pro	Val	Lys	Trp	Leu	Ala	680	685	690
10	Leu	Glu	Ser	Leu	Ala	Asp	Asn	Leu	Tyr	Thr	Val	His	Ser	Asp	Val	695	700	705
	Trp	Ala	Phe	Gly	Val	Thr	Met	Trp	Glu	Ile	Met	Thr	Arg	Gly	Gln	710	715	720
15	Thr	Pro	Tyr	Ala	Gly	Ile	Glu	Asn	Ala	Glu	Ile	Tyr	Asn	Tyr	Leu	725	730	735
	Ile	Gly	Gly	Asn	Arg	Leu	Lys	Gln	Pro	Pro	Glu	Cys	Met	Glu	Glu	740	745	750
20	Val	Tyr	Asp	Leu	Met	Tyr	Gln	Cys	Trp	Ser	Ala	Asp	Pro	Lys	Gln	755	760	765
	Arg	Pro	Ser	Phe	Thr	Cys	Leu	Arg	Met	Glu	Leu	Glu	Asn	Ile	Leu	770	775	780
	Gly	His	Leu	Ser	Val	Leu	Ser	Thr	Ser	Gln	Asp	Pro	Leu	Tyr	Ile	785	790	795
30	Asn	Ile	Glu	Arg	Ala	Glu	Gln	Pro	Thr	Glu	Ser	Gly	Ser	Pro	Glu	800	805	810
	Leu	His	Cys	Gly	Glu	Arg	Ser	Ser	Ser	Glu	Ala	Gly	Asp	Gly	Ser	815	820	825
35	Gly	Val	Gly	Ala	Val	Gly	Gly	Ile	Pro	Ser	Asp	Ser	Arg	Tyr	Ile	830	835	840
	Phe	Ser	Pro	Gly	Gly	Leu	Ser	Glu	Ser	Pro	Gly	Gln	Leu	Glu	Gln	845	850	855
40	Gln	Pro	Glu	Ser	Pro	Leu	Asn	Glu	Asn	Gln	Arg	Leu	Leu	Leu	Leu	860	865	870
45	Gln	Gln	Gly	Leu	Leu	Pro	His	Ser	Ser	Cys	875	880						

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1164 bases



(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCAGGCCTGA AGCTCATGGG CGCCCCAGTG AAGATGACCG TGTCTCAGGG 50  
10 GCAGCCAGTG AAGCTCAACT GCAGCGTGGA GGGGATGGAG GACCCTGACA 100  
TCCACTGGAT GAAGGATGGC ACCGTGGTCC AGAATGCAAG CCAGGTGTCC 150  
15 ATCTCCATCA GCGAGCACAG CTGGATTGGC TTACTCAGCC TAAAGTCAGT 200  
GGAGCGGTCT GATGCTGGCC TGTACTGGTG CCAGGTGAAG GATGGGGAGG 250  
20 AAACCAAGAT CTCTCAGTCA GTATGGCTCA CTGTCGAAGG TGTGCCATTTC 300  
25 TTCACAGTGG AACCAAAAGA TCTGGCGGTG CCACCCAATG CCCCTTTTCA 350  
GCTGTCTTGT GAGGCTGTGG GTCCTCCAGA ACCCGTAACC ATTTACTGGT 400  
30 GGAGAGGACT CACTAAGGTT GGGGGACCTG CTCCCTCTCC CTCTGTTTTA 450  
AATGTGACAG GAGTGACCCA GCGCACAGAG TTTTCTTGTG AAGCCCGCAA 500  
35 CATAAAAGGC CTGGCCACTT CCCGACCAGC CATTGTTCGC CTTCAAGCAC 550  
40 CGCCTGCAGC TCCTTTCAAC ACCACAGTAA CAACGATCTC CAGCTACAAC 600  
GCTAGCGTGG CCTGGGTGCC AGGTGCTGAC GGCCTAGCTC TGCTGCATTTC 650  
45 CTGTACTGTA CAGGTGGCAC ACGCCCCAGG AGAATGGGAG GCCCTTGCTG 700  
50 TTGTGGTTCC TGTGCCACCT TTTACCTGCC TGCTTCGGAA CTTGGCCCCT 750

GCCACCAACT ACAGCCTTAG GGTGCGCTGT GCCAATGCCT TGGGCCCTTC 800  
 TCCCTACGGC GACTGGGTGC CCTTTCAGAC AAAGGGCCTA GCGCCAGCCA 850  
 GAGCTCCTCA GAATTTCCAT GCCATTCGTA CCGACTCAGG CCTTATCCTG 900  
 GAATGGGAAG AAGTGATTCC TGAAGACCCT GGGGAAGGCC CCCTAGGACC 950  
 TTATAAGCTG TCCTGGGTCC AAGAAAATGG AACCCAGGAT GAGCTGATGG 1000  
 TGGAAGGGAC CAGGGCCAAT CTGACCGACT GGGATCCCCA GAAGGACCTG 1050  
 ATTTTGCGTG TGTGTGCCTC CAATGCAATT GGTGATGGGC CCTGGAGTCA 1100  
 GCCACTGGTG GTGTCTTCTC ATGACCATGC AGGGAGGCAG GGCCCTCCCC 1150  
 ACAGCCGCAC ATCC 1164

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala	Gly	Leu	Lys	Leu	Met	Gly	Ala	Pro	Val	Lys	Met	Thr	Val	Ser
1				5					10					15
Gln	Gly	Gln	Pro	Val	Lys	Leu	Asn	Cys	Ser	Val	Glu	Gly	Met	Glu
			20						25					30
Asp	Pro	Asp	Ile	His	Trp	Met	Lys	Asp	Gly	Thr	Val	Val	Gln	Asn
			35						40					45
Ala	Ser	Gln	Val	Ser	Ile	Ser	Ile	Ser	Glu	His	Ser	Trp	Ile	Gly
			50						55					60
Leu	Leu	Ser	Leu	Lys	Ser	Val	Glu	Arg	Ser	Asp	Ala	Gly	Leu	Tyr
			65						70					75

	Trp	Cys	Gln	Val	Lys	Asp	Gly	Glu	Glu	Thr	Lys	Ile	Ser	Gln	Ser	80	85	90
5	Val	Trp	Leu	Thr	Val	Glu	Gly	Val	Pro	Phe	Phe	Thr	Val	Glu	Pro	95	100	105
	Lys	Asp	Leu	Ala	Val	Pro	Pro	Asn	Ala	Pro	Phe	Gln	Leu	Ser	Cys	110	115	120
10	Glu	Ala	Val	Gly	Pro	Pro	Glu	Pro	Val	Thr	Ile	Tyr	Trp	Trp	Arg	125	130	135
	Gly	Leu	Thr	Lys	Val	Gly	Gly	Pro	Ala	Pro	Ser	Pro	Ser	Val	Leu	140	145	150
15	Asn	Val	Thr	Gly	Val	Thr	Gln	Arg	Thr	Glu	Phe	Ser	Cys	Glu	Ala	155	160	165
20	Arg	Asn	Ile	Lys	Gly	Leu	Ala	Thr	Ser	Arg	Pro	Ala	Ile	Val	Arg	170	175	180
	Leu	Gln	Ala	Pro	Pro	Ala	Ala	Pro	Phe	Asn	Thr	Thr	Val	Thr	Thr	185	190	195
25	Ile	Ser	Ser	Tyr	Asn	Ala	Ser	Val	Ala	Trp	Val	Pro	Gly	Ala	Asp	200	205	210
	Gly	Leu	Ala	Leu	Leu	His	Ser	Cys	Thr	Val	Gln	Val	Ala	His	Ala	215	220	225
30	Pro	Gly	Glu	Trp	Glu	Ala	Leu	Ala	Val	Val	Val	Pro	Val	Pro	Pro	230	235	240
35	Phe	Thr	Cys	Leu	Leu	Arg	Asn	Leu	Ala	Pro	Ala	Thr	Asn	Tyr	Ser	245	250	255
	Leu	Arg	Val	Arg	Cys	Ala	Asn	Ala	Leu	Gly	Pro	Ser	Pro	Tyr	Gly	260	265	270
40	Asp	Trp	Val	Pro	Phe	Gln	Thr	Lys	Gly	Leu	Ala	Pro	Ala	Arg	Ala	275	280	285
	Pro	Gln	Asn	Phe	His	Ala	Ile	Arg	Thr	Asp	Ser	Gly	Leu	Ile	Leu	290	295	300
45	Glu	Trp	Glu	Glu	Val	Ile	Pro	Glu	Asp	Pro	Gly	Glu	Gly	Pro	Leu	305	310	315
50	Gly	Pro	Tyr	Lys	Leu	Ser	Trp	Val	Gln	Glu	Asn	Gly	Thr	Gln	Asp	320	325	330

Glu	Leu	Met	Val	Glu	Gly	Thr	Arg	Ala	Asn	Leu	Thr	Asp	Trp	Asp
				335					340					345
Pro	Gln	Lys	Asp	Leu	Ile	Leu	Arg	Val	Cys	Ala	Ser	Asn	Ala	Ile
				350					355					360
Gly	Asp	Gly	Pro	Trp	Ser	Gln	Pro	Leu	Val	Val	Ser	Ser	His	Asp
				365					370					375
His	Ala	Gly	Arg	Gln	Gly	Pro	Pro	His	Ser	Arg	Thr	Ser		
				380					385			388		

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGGATCCACA CGATGCGACT CTT 23

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAATTCCTC TCATGGAGCT AGTCCATCTC T 31

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGATCCATC CACAGAGATG T 21

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGAATTCCAA AGGACCAGCA CGATC 25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACCGTGTGT GTGGCTGACT TTGGACTCTC CTGGAAGATC 40

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCTGTGCCT CCAAATTGCC CGTCAAGTGG CTGGCCCTGG 40

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCCGGTGAA GCTGAACTGC AGTGTGGAGG GGATGGAGGA GCCTGACATC 50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCCAGCTACA ACGCTAGCGT GGCCTGGGTG CCAGGTGCTG ACGGCCTAGC 50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile His Arg Asp Leu Ala Ala Arg Asn  
1 5 9

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Trp Ile Ala Ile Glu  
1 5 6

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Thr Trp Thr Met Ala Pro Glu  
1 5 8

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Trp Leu Ala Leu Glu  
1 5 6

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Lys Trp Met Ala Leu Glu  
1 5 6

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGCTGCTCG AGGCAGGTCT GAAGCTCATG 30

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCATGAATTC ATGGCACACC TTCTACCGTG 30

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CACTGAGCTG GCTGACTAAG 20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCTGATAGGC TGGGTACTCC 20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAGCCCGGAC TGACCAA 18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTGCGGAATC AGAAAGATGG 20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCAAGACAAT GGAACCCA 18

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CATGGAATTC GGTGACCGAT GTGCGGCTGT GAGGAG 36

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 894 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

0	Met	Ala	Trp	Arg	Cys	Pro	Arg	Met	Gly	Arg	Val	Pro	Leu	Ala	Trp	
	1				5				10						15	
	Cys	Leu	Ala	Leu	Cys	Gly	Trp	Ala	Cys	Met	Ala	Pro	Arg	Gly	Thr	
					20				25						30	
5	Gln	Ala	Glu	Glu	Ser	Pro	Phe	Val	Gly	Asn	Pro	Gly	Asn	Ile	Thr	
					35				40						45	
0	Gly	Ala	Arg	Gly	Leu	Thr	Gly	Thr	Leu	Arg	Cys	Gln	Leu	Gln	Val	
					50				55						60	
	Gln	Gly	Glu	Pro	Pro	Glu	Val	His	Trp	Leu	Arg	Asp	Gly	Gln	Ile	
					65				70						75	
5	Leu	Glu	Leu	Ala	Asp	Ser	Thr	Gln	Thr	Gln	Val	Pro	Leu	Gly	Glu	
					80				85						90	
	Asp	Glu	Gln	Asp	Asp	Trp	Ile	Val	Val	Ser	Gln	Leu	Arg	Ile	Thr	
					95				100						105	
0	Ser	Leu	Gln	Leu	Ser	Asp	Thr	Gly	Gln	Tyr	Gln	Cys	Leu	Val	Phe	
					110				115						120	
	Leu	Gly	His	Gln	Thr	Phe	Val	Ser	Gln	Pro	Gly	Tyr	Val	Gly	Leu	
5					125				130						135	
	Glu	Gly	Leu	Pro	Tyr	Phe	Leu	Glu	Glu	Pro	Glu	Asp	Arg	Thr	Val	
					140				145						150	
0	Ala	Ala	Asn	Thr	Pro	Phe	Asn	Leu	Ser	Cys	Gln	Ala	Gln	Gly	Pro	
					155				160						165	
	Pro	Glu	Pro	Val	Asp	Leu	Leu	Trp	Leu	Gln	Asp	Ala	Val	Pro	Leu	
					170				175						180	
5	Ala	Thr	Ala	Pro	Gly	His	Gly	Pro	Gln	Arg	Ser	Leu	His	Val	Pro	
					185				190						195	
0	Gly	Leu	Asn	Lys	Thr	Ser	Ser	Phe	Ser	Cys	Glu	Ala	His	Asn	Ala	
					200				205						210	

	Lys	Gly	Val	Thr	Thr	Ser	Arg	Thr	Ala	Thr	Ile	Thr	Val	Leu	Pro
					215					220					225
5	Gln	Gln	Pro	Arg	Asn	Leu	His	Leu	Val	Ser	Arg	Gln	Pro	Thr	Glu
					230					235					240
	Leu	Glu	Val	Ala	Trp	Thr	Pro	Gly	Leu	Ser	Gly	Ile	Tyr	Pro	Leu
					245					250					255
0	Thr	His	Cys	Thr	Leu	Gln	Ala	Val	Leu	Ser	Asp	Asp	Gly	Met	Gly
					260					265					270
	Ile	Gln	Ala	Gly	Glu	Pro	Asp	Pro	Pro	Glu	Glu	Pro	Leu	Thr	Ser
5					275					280					285
	Gln	Ala	Ser	Val	Pro	Pro	His	Gln	Leu	Arg	Leu	Gly	Ser	Leu	His
					290					295					300
0	Pro	His	Thr	Pro	Tyr	His	Ile	Arg	Val	Ala	Cys	Thr	Ser	Ser	Gln
					305					310					315
	Gly	Pro	Ser	Ser	Trp	Thr	His	Trp	Leu	Pro	Val	Glu	Thr	Pro	Glu
					320					325					330
5	Gly	Val	Pro	Leu	Gly	Pro	Pro	Glu	Asn	Ile	Ser	Ala	Thr	Arg	Asn
					335					340					345
	Gly	Ser	Gln	Ala	Phe	Val	His	Trp	Gln	Glu	Pro	Arg	Ala	Pro	Leu
0					350					355					360
	Gln	Gly	Thr	Leu	Leu	Gly	Tyr	Arg	Leu	Ala	Tyr	Gln	Gly	Gln	Asp
					365					370					375
5	Thr	Pro	Glu	Val	Leu	Met	Asp	Ile	Gly	Leu	Arg	Gln	Glu	Val	Thr
					380					385					390
	Leu	Glu	Leu	Gln	Gly	Asp	Gly	Ser	Val	Ser	Asn	Leu	Thr	Val	Cys
					395					400					405
0	Val	Ala	Ala	Tyr	Thr	Ala	Ala	Gly	Asp	Gly	Pro	Trp	Ser	Leu	Pro
					410					415					420
	Val	Pro	Leu	Glu	Ala	Trp	Arg	Pro	Gly	Gln	Ala	Gln	Pro	Val	His
5					425					430					435
	Gln	Leu	Val	Lys	Glu	Pro	Ser	Thr	Pro	Ala	Phe	Ser	Trp	Pro	Trp
					440					445					450
0	Trp	Tyr	Val	Leu	Leu	Gly	Ala	Val	Val	Ala	Ala	Ala	Cys	Val	Leu
					455					460					465

	Ile	Leu	Ala	Leu	Phe 470	Leu	Val	His	Arg	Arg 475	Lys	Lys	Glu	Thr	Arg 480
5	Tyr	Gly	Glu	Val	Phe 485	Glu	Pro	Thr	Val	Glu 490	Arg	Gly	Glu	Leu	Val 495
	Val	Arg	Tyr	Arg	Val 500	Arg	Lys	Ser	Tyr	Ser 505	Arg	Arg	Thr	Thr	Glu 510
0	Ala	Thr	Leu	Asn	Ser 515	Leu	Gly	Ile	Ser	Glu 520	Glu	Leu	Lys	Glu	Lys 525
	Leu	Arg	Asp	Val	Met 530	Val	Asp	Arg	His	Lys 535	Val	Ala	Leu	Gly	Lys 540
5	Thr	Leu	Gly	Glu	Gly 545	Glu	Phe	Gly	Ala	Val 550	Met	Glu	Gly	Gln	Leu 555
0	Asn	Gln	Asp	Asp	Ser 560	Ile	Leu	Lys	Val	Ala 565	Val	Lys	Thr	Met	Lys 570
	Ile	Ala	Ile	Cys	Thr 575	Arg	Ser	Glu	Leu	Glu 580	Asp	Phe	Leu	Ser	Glu 585
5	Ala	Val	Cys	Met	Lys 590	Glu	Phe	Asp	His	Pro 595	Asn	Val	Met	Arg	Leu 600
	Ile	Gly	Val	Cys	Phe 605	Gln	Gly	Ser	Glu	Arg 610	Glu	Ser	Phe	Pro	Ala 615
0	Pro	Val	Val	Ile	Leu 620	Pro	Phe	Met	Lys	His 625	Gly	Asp	Leu	His	Ser 630
5	Phe	Leu	Leu	Tyr	Ser 635	Arg	Leu	Gly	Asp	Gln 640	Pro	Val	Tyr	Leu	Pro 645
	Thr	Gln	Met	Leu	Val 650	Lys	Phe	Met	Ala	Asp 655	Ile	Ala	Ser	Gly	Met 660
0	Glu	Tyr	Leu	Ser	Thr 665	Lys	Arg	Phe	Ile	His 670	Arg	Asp	Leu	Ala	Ala 675
	Arg	Asn	Cys	Met	Leu 680	Asn	Glu	Asn	Met	Ser 685	Val	Cys	Val	Ala	Asp 690
5	Phe	Gly	Leu	Ser	Lys 695	Lys	Ile	Tyr	Asn	Gly 700	Asp	Tyr	Tyr	Arg	Gln 705
10	Gly	Arg	Ile	Ala	Lys 710	Met	Pro	Val	Lys	Trp 715	Ile	Ala	Ile	Glu	Ser 720

	Leu	Ala	Asp	Arg	Val	Tyr	Thr	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	725	730	735
5	Gly	Val	Thr	Met	Trp	Glu	Ile	Ala	Thr	Arg	Gly	Gln	Thr	Pro	Tyr	740	745	750
	Pro	Gly	Val	Glu	Asn	Ser	Glu	Ile	Tyr	Asp	Tyr	Leu	Arg	Gln	Gly	755	760	765
0	Asn	Arg	Leu	Lys	Gln	Pro	Ala	Asp	Cys	Leu	Asp	Gly	Leu	Tyr	Ala	770	775	780
	Leu	Met	Ser	Arg	Cys	Trp	Glu	Leu	Asn	Pro	Gln	Asp	Arg	Pro	Ser	785	790	795
5	Phe	Thr	Glu	Leu	Arg	Glu	Asp	Leu	Glu	Asn	Thr	Leu	Lys	Ala	Leu	800	805	810
	Pro	Pro	Ala	Gln	Glu	Pro	Asp	Glu	Ile	Leu	Tyr	Val	Asn	Met	Asp	815	820	825
0	Glu	Gly	Gly	Gly	Tyr	Pro	Glu	Pro	Pro	Gly	Ala	Ala	Gly	Gly	Ala	830	835	840
5	Asp	Pro	Pro	Thr	Gln	Pro	Asp	Pro	Lys	Asp	Ser	Cys	Ser	Cys	Leu	845	850	855
	Thr	Ala	Ala	Glu	Val	His	Pro	Ala	Gly	Arg	Tyr	Val	Leu	Cys	Pro	860	865	870
0	Ser	Thr	Thr	Pro	Ser	Pro	Ala	Gln	Pro	Ala	Asp	Arg	Gly	Ser	Pro	875	880	885
5	Ala	Ala	Pro	Gly	Gln	Glu	Asp	Gly	Ala							890		894

(2) INFORMATION FOR SEQ ID NO:35:

0 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 888 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

	Met	Gly	Arg	Val	Pro	Leu	Ala	Trp	Trp	Leu	Ala	Leu	Cys	Cys	Trp	1	5	10	15
10	Gly	Cys	Ala	Ala	His	Lys	Asp	Thr	Gln	Thr	Glu	Ala	Gly	Ser	Pro	20	25	30	

	Phe	Val	Gly	Asn	Pro	Gly	Asn	Ile	Thr	Gly	Ala	Arg	Gly	Leu	Thr	
					35					40					45	
5	Gly	Thr	Leu	Arg	Cys	Glu	Leu	Gln	Val	Gln	Gly	Glu	Pro	Pro	Glu	
					50					55					60	
	Val	Val	Trp	Leu	Arg	Asp	Gly	Gln	Ile	Leu	Glu	Leu	Ala	Asp	Asn	
					65					70					75	
0	Thr	Gln	Thr	Gln	Val	Pro	Leu	Gly	Glu	Asp	Trp	Gln	Asp	Glu	Trp	
					80					85					90	
	Lys	Val	Val	Ser	Gln	Leu	Arg	Ile	Ser	Ala	Leu	Gln	Leu	Ser	Asp	
					95					100					105	
5	Ala	Gly	Glu	Tyr	Gln	Cys	Met	Val	His	Leu	Glu	Gly	Arg	Thr	Phe	
					110					115					120	
0	Val	Ser	Gln	Pro	Gly	Phe	Val	Gly	Leu	Glu	Gly	Leu	Pro	Tyr	Phe	
					125					130					135	
	Leu	Glu	Glu	Pro	Glu	Asp	Lys	Ala	Val	Pro	Ala	Asn	Thr	Pro	Phe	
					140					145					150	
5	Asn	Leu	Ser	Cys	Gln	Ala	Gln	Gly	Pro	Pro	Glu	Pro	Val	Thr	Leu	
					155					160					165	
	Leu	Trp	Leu	Gln	Asp	Ala	Val	Pro	Leu	Ala	Pro	Val	Thr	Gly	His	
					170					175					180	
0	Ser	Ser	Gln	His	Ser	Leu	Gln	Thr	Pro	Gly	Leu	Asn	Lys	Thr	Ser	
					185					190					195	
	Ser	Phe	Ser	Cys	Glu	Ala	His	Asn	Ala	Lys	Gly	Val	Thr	Thr	Ser	
5					200					205					210	
	Arg	Thr	Ala	Thr	Ile	Thr	Val	Leu	Pro	Gln	Arg	Pro	His	His	Leu	
					215					220					225	
0	His	Val	Val	Ser	Arg	Gln	Pro	Thr	Glu	Leu	Glu	Val	Ala	Trp	Thr	
					230					235					240	
	Pro	Gly	Leu	Ser	Gly	Ile	Tyr	Pro	Leu	Thr	His	Cys	Asn	Leu	Gln	
					245					250					255	
5	Ala	Val	Leu	Ser	Asp	Asp	Gly	Val	Gly	Ile	Trp	Leu	Gly	Lys	Ser	
					260					265					270	
0	Asp	Pro	Pro	Glu	Asp	Pro	Leu	Thr	Leu	Gln	Val	Ser	Val	Pro	Pro	
					275					280					285	

	His	Gln	Leu	Arg	Leu	Glu	Lys	Leu	Leu	Pro	His	Thr	Pro	Tyr	His	
					290					295					300	
5	Ile	Arg	Ile	Ser	Cys	Ser	Ser	Ser	Gln	Gly	Pro	Ser	Pro	Trp	Thr	
					305					310					315	
	His	Trp	Leu	Pro	Val	Glu	Thr	Thr	Glu	Gly	Val	Pro	Leu	Gly	Pro	
					320					325					330	
0	Pro	Glu	Asn	Val	Ser	Ala	Met	Arg	Asn	Gly	Ser	Gln	Val	Leu	Val	
					335					340					345	
	Arg	Trp	Gln	Glu	Pro	Arg	Val	Pro	Leu	Gln	Gly	Thr	Leu	Leu	Gly	
5					350					355					360	
	Tyr	Arg	Leu	Ala	Tyr	Arg	Gly	Gln	Asp	Thr	Pro	Glu	Val	Leu	Met	
					365					370					375	
0	Asp	Ile	Gly	Leu	Thr	Arg	Glu	Val	Thr	Leu	Glu	Leu	Arg	Gly	Asp	
					380					385					390	
	Arg	Pro	Val	Ala	Asn	Leu	Thr	Val	Ser	Val	Thr	Ala	Tyr	Thr	Ser	
					395					400					405	
5	Ala	Gly	Asp	Gly	Pro	Trp	Ser	Leu	Pro	Val	Pro	Leu	Glu	Pro	Trp	
					410					415					420	
	Arg	Pro	Gly	Gln	Gly	Gln	Pro	Leu	His	His	Leu	Val	Ser	Glu	Pro	
0					425					430					435	
	Pro	Pro	Arg	Ala	Phe	Ser	Trp	Pro	Trp	Trp	Tyr	Val	Leu	Leu	Gly	
					440					445					450	
5	Ala	Leu	Val	Ala	Ala	Ala	Cys	Val	Leu	Ile	Leu	Ala	Leu	Phe	Leu	
					455					460					465	
	Val	His	Arg	Arg	Lys	Lys	Glu	Thr	Arg	Tyr	Gly	Glu	Val	Phe	Glu	
					470					475					480	
0	Pro	Thr	Val	Glu	Arg	Gly	Glu	Leu	Val	Val	Arg	Tyr	Arg	Val	Arg	
					485					490					495	
	Lys	Ser	Tyr	Ser	Arg	Arg	Thr	Thr	Glu	Ala	Thr	Leu	Asn	Ser	Leu	
5					500					505					510	
	Gly	Ile	Ser	Glu	Glu	Leu	Lys	Glu	Lys	Leu	Arg	Asp	Val	Met	Val	
					515					520					525	
0	Asp	Arg	His	Lys	Val	Ala	Leu	Gly	Lys	Thr	Leu	Gly	Glu	Gly	Glu	
					530					535					540	

	Phe Gly Ala Val	Met Glu Gly Gln Leu	Asn Gln Asp Asp Ser	Ile
		545	550	555
5	Leu Lys Val Ala	Val Lys Thr Met Lys	Ile Ala Ile Cys Thr	Arg
		560	565	570
	Ser Glu Leu Glu	Asp Phe Leu Ser Glu	Ala Val Cys Met Lys	Glu
		575	580	585
0	Phe Asp His Pro	Asn Val Met Arg Leu	Ile Gly Val Cys Phe	Gln
		590	595	600
	Gly Ser Asp Arg	Glu Gly Phe Pro Glu	Pro Val Val Ile Leu	Pro
		605	610	615
5	Phe Met Lys His	Gly Asp Leu His Ser	Phe Leu Leu Tyr Ser	Arg
		620	625	630
	Leu Gly Asp Gln	Pro Val Phe Leu Pro	Thr Gln Met Leu Val	Lys
0		635	640	645
	Phe Met Ala Asp	Ile Ala Ser Gly Met	Glu Tyr Leu Ser Thr	Lys
		650	655	660
5	Arg Phe Ile His	Arg Asp Leu Ala Ala	Arg Asn Cys Met Leu	Asn
		665	670	675
	Glu Asn Met Ser	Val Cys Val Ala Asp	Phe Gly Leu Ser Lys	Lys
		680	685	690
0	Ile Tyr Asn Gly	Asp Tyr Tyr Arg Gln	Gly Arg Ile Ala Lys	Met
		695	700	705
	Pro Val Lys Trp	Ile Ala Ile Glu Ser	Leu Ala Asp Arg Val	Tyr
5		710	715	720
	Thr Ser Lys Ser	Asp Val Trp Ser Phe	Gly Val Thr Met Trp	Glu
		725	730	735
0	Ile Ala Thr Arg	Gly Gln Thr Pro Tyr	Pro Gly Val Glu Asn	Ser
		740	745	750
	Glu Ile Tyr Asp	Tyr Leu Arg Gln Gly	Asn Arg Leu Lys Gln	Pro
		755	760	765
5	Val Asp Phe Leu	Asp Gly Leu Tyr Ser	Leu Met Ser Arg Cys	Trp
		770	775	780
	Glu Leu Asn Pro	Arg Asp Arg Pro Ser	Phe Ala Glu Leu Arg	Glu
0		785	790	795



	Asp	Leu	Glu	Asn	Thr	Leu	Lys	Ala	Leu	Pro	Pro	Ala	Gln	Glu	Pro
					800					805					810
5	Asp	Glu	Ile	Leu	Tyr	Val	Asn	Met	Asp	Glu	Gly	Gly	Ser	His	Leu
					815					820					825
	Glu	Pro	Arg	Gly	Ala	Ala	Gly	Gly	Ala	Asp	Pro	Pro	Thr	Gln	Pro
					830					835					840
0	Asp	Pro	Lys	Asp	Ser	Cys	Ser	Cys	Leu	Thr	Ala	Ala	Asp	Val	His
					845					850					855
	Ser	Ala	Gly	Arg	Tyr	Val	Leu	Cys	Pro	Ser	Thr	Ala	Pro	Gly	Pro
5					860					865					870
	Thr	Leu	Ser	Ala	Asp	Arg	Gly	Cys	Pro	Ala	Pro	Pro	Gly	Gln	Glu
					875					880					885
0	Asp	Gly	Ala												
					888										